

FO990" 59554860

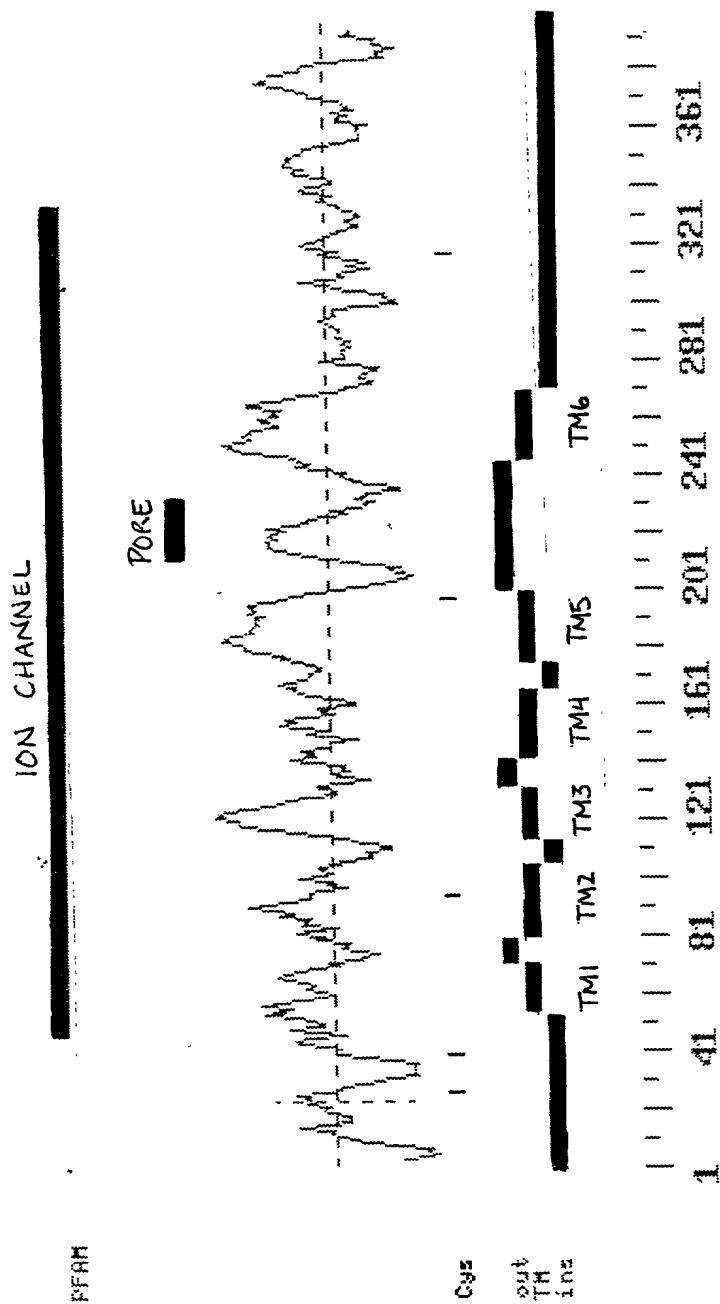


Figure 1

CLUSTAL W (1.74) multiple sequence alignment

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Fbh56201pat -----
hSCN4A      MARPSLCTLVPLGPECLRPFTRESLAAIEQRAVEEEEARLQRNKQMEIEEPEKPRSDLEA

Fbh56201pat -----
hSCN4A      GKNLPMIYGDPPPEVIGIPLEDLDPYYSNKKTFFIVLNKGKAIFRFSATPALYLLSPFSVV

Fbh56201pat -----
hSCN4A      RRGAIKVLIIHALFSMEIMITILTNCVFM TMSDPPPWSKNVEYFTFTGIYTFESLIKILARG

Fbh56201pat -----
hSCN4A      FCVDDFTFLRDPWNWLD FSVIMMAYLTEFVDLGNISALRTFRVLRALKTTITVIPGLKTIV

Fbh56201pat -----
hSCN4A      GALIQSVKKLS DVMILT VFCLSVFALVGLQLFMGNLRQKCVRWPPPFNDTNTTWYSNDTW

Fbh56201pat -----
hSCN4A      YGNDTWYGNEMWYGND SWYANDTWNSHASWATNDTFDWDAYISDEGNFYFLEGSNDALLC

Fbh56201pat -----
hSCN4A      GNSSDAGHCPQGYECIKTGRNPNGYGYTSYDTFSWAFLALFRLMTQDYWENLFQLT LRAAG

Fbh56201pat -----
hSCN4A      KTYMIFVVIIFLGSFYLINLILAVVAMAYAEQNEATLAEDKEKEEEFQQM LEKFKKHQE

Fbh56201pat -----
hSCN4A      ELEKAKAAQALEGGEADGDPAHGKDCNGSLDTSQGEKGAPRQSGSGDSGISDAMEEELEEA

Fbh56201pat -----
hSCN4A      HQKCPPWWYKCAHKVLIWNCCAPWLKFKNIIHLIVMDPFVDLGITICIVLNTLFMAMEHY

Fbh56201pat -----
hSCN4A      PMTEHFDNVLT VGNLVFTGIFTAEMVLKLIAMD PYEYFQQGWNI FDSII VTL SLVELGLA

Fbh56201pat -----
hSCN4A      NVQGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQ

Fbh56201pat -----
hSCN4A      LFGKSYKECVCKIALDCNLPRWHMHDFH SFLIVFRILCGEWIETMWDCMEVAGQAMCLT

Fbh56201pat -----
hSCN4A      VFLMVMVIGNLVVLNLFLALLLSSFSADSLAASDEDGEMNNLQIAIGRIKLGIGFAKAFI

Fbh56201pat -----

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Figure 3 (1 of 3)

[illegible]

Figure 3 (2 of 3)

hSCN4A

AYRRHLLQRSMKQASYMYRSHDGSDDAPEKEGLLANTMSKMYGHENGSSSPSPEEKG

Fbh56201pat
hSCN4A

EAGDAGPTMGLMPISPSDTAWPPAPPPGQTVRPGVKESLV

Figure 3 (3 of 3)